

## Best Available Copy

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Gencore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 18, 2001, 00:04:02 ; Search time 1176.35 Seconds  
(without alignments)

2892.870 Million cell updates/sec

Title: US-09-457-066-1\_COPY\_829\_1188

Perfect score: 360

Sequence: 1 gcttttttttggaaat.....gcagaggagacaggagga 360

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: qb\_est1:\*

2: qb\_est2:\*

3: qb\_est3:\*

4: qb\_est4:\*

5: qb\_est5:\*

6: qb\_est6:\*

7: qb\_est7:\*

8: qb\_est8:\*

9: qb\_est9:\*

10: qb\_est10:\*

11: qb\_est11:\*

12: qb\_est12:\*

13: qb\_est13:\*

14: qb\_est14:\*

15: qb\_est15:\*

16: qb\_est16:\*

17: qb\_est17:\*

18: qb\_est18:\*

19: qb\_est19:\*

20: qb\_est20:\*

21: qb\_est21:\*

22: qb\_est22:\*

23: qb\_est23:\*

24: qb\_est24:\*

25: qb\_est33:\*

26: qb\_est34:\*

27: qb\_est35:\*

28: qb\_est36:\*

29: qb\_est37:\*

30: qb\_est38:\*

31: qb\_est39:\*

32: qb\_est40:\*

33: em\_estba:\*

34: em\_estfun:\*

35: em\_esthum1:\*

36: em\_esthum2:\*

37: em\_esthum3:\*

38: em\_esthum4:\*

39: em\_esthum5:\*

40: em\_esthum6:\*

41: em\_esthum7:\*

42: em\_esthum8:\*

43: em\_esthum9:\*

44: em\_esthum10:\*

45: em\_esthum11:\*

46: em\_esthum12:\*

47: em\_esthum13:\*

48: em\_esthum14:\*

49: em\_esthum15:\*

50: em\_esthum16:\*

51: em\_esthum17:\*

52: em\_esthum18:\*

53: em\_esthum19:\*

54: em\_esthum20:\*

55: em\_esthum21:\*

56: em\_esthum22:\*

57: em\_esthum23:\*

58: em\_esthum24:\*

59: em\_esthum25:\*

60: em\_esthum26:\*

61: em\_esthum27:\*

62: em\_esthum28:\*

63: em\_estin1:\*

64: em\_estin2:\*

65: em\_estin3:\*

66: em\_estin4:\*

67: em\_estin5:\*

68: em\_estcom1:\*

69: em\_estcom2:\*

70: em\_estcov1:\*

71: em\_estcov2:\*

72: em\_estp11:\*

73: em\_estp12:\*

74: em\_estp13:\*

75: em\_estp14:\*

76: em\_estp15:\*

77: em\_estp16:\*

78: em\_estp17:\*

79: em\_estp18:\*

80: em\_estp19:\*

81: em\_estp110:\*

82: em\_estr01:\*

83: em\_estr02:\*

84: em\_estr03:\*

85: em\_estr04:\*

86: em\_estr05:\*

87: em\_estr06:\*

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93: em\_estr012:\*

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95: em\_estr04:\*

96: em\_estr05:\*

97: em\_estr06:\*

98: em\_estr07:\*

99: em\_estr08:\*

100: em\_estr09:\*

101: em\_estr010:\*

102: qb\_est25:\*

103: qb\_est26:\*

104: qb\_est27:\*

105: qb\_est28:\*

106: qb\_est29:\*

107: qb\_est30:\*

108: qb\_est31:\*

109: qb\_est32:\*

110: qb\_est41:\*

111: qb\_est42:\*

112: qb\_est43:\*

113: qb\_est44:\*

114: qb\_est45:\*

115: qb\_est46:\*

116: qb\_est47:\*

## Best Available Copy

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117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
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175: gb_est98:*
176: gb_est99:*
177: em_esthnum29:*
178: em_esthnum30:*
179: em_esthnum31:*
180: em_esthnum32:*
181: em_esthnum33:*
182: em_estp111:*
183: em_estro21:*
184: em_estro22:*
185: em_estro23:*
186: em_htc:*
187: gb_est107:*
188: gb_est108:*
189: gb_est109:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Best Available Copy

## SUMMARIES

Result	Result No.	Score	Query	Match	Length	DB ID	Description
1	343	8.95.5	BB958470	BB958470	142	BE958470	6016447870
2	302	8.94.0	AL047637	AL047637	105	AL047637	DKT2P586J
3	302	8.93.9	BF102899	BF102899	144	BF102899	601646827
4	283	8.978.8	BF031624	BF031624	950	BF031624	601558104
5	274	8.976.2	BF021679	BF021679	523	BF021679	BF021679
6	265	8.973.7	BF609411	BF609411	556	BF609411	BF609411
7	255	8.972.7	BF151355	BF151355	564	BF151355	BF151355
8	255	8.971.8	BF670092	BF670092	168	BF670092	BF670092
9	250	8.969.5	BF243001	BF243001	910	BF243001	602355974
10	230	8.963.9	BF011835	BF011835	143	BF011835	BF011835
11	209	8.958.2	BF118707	BF118707	174	BF118707	BF118707
c	158	8.944.0	BF163629	BF163629	902	BF163629	BF163629
c	141	8.939.3	BF1769732	BF1769732	145	BF1769732	BF1769732
c	14	8.939.6	AA759138	AA759138	425	AA759138	AA759138
c	14	8.938.8	BE374398	BE374398	521	BE374398	BE374398
c	15	8.932.9	AI020581	AI020581	324	AI020581	AI020581
c	16	8.932.4	BF0180978	BF0180978	322	BF0180978	BF0180978
c	17	8.932.4	CNS024633	CNS024633	337	CNS024633	CNS024633
c	18	8.932.3	AW167653	AW167653	112	AW167653	AW167653
c	19	8.926.4	AI024617	AI024617	389	AI024617	AI024617
c	20	8.926.3	AW210331	AW210331	511	AW210331	AW210331
c	21	8.924.8	BF117246	BF117246	126	BF117246	BF117246
c	22	8.924.7	AI470494	AI470494	354	AI470494	AI470494
c	23	8.923.8	AK003359	AK003359	1796	AK003359	AK003359
c	24	8.923.7	Mus muscu	Mus muscu	192	Mus muscu	Mus muscu
c	25	8.921.0	HW582850	HW582850	1036	HW582850	HW582850
c	26	8.919.4	RC1-ST027	RC1-ST027	193	RC1-ST027	RC1-ST027
c	27	8.919.6	AL304867	AL304867	155	AL304867	AL304867
c	28	8.915.1	BF143048	BF143048	142	BF143048	BF143048
c	29	8.914.7	BE937452	BE937452	165	BE937452	BE937452
c	30	8.911.4	BF289243	BF289243	165	BF289243	BF289243
c	31	8.910.8	BE289243	BE289243	165	BE289243	BE289243
c	32	8.910.2	W21436	W21436	190	W21436	W21436
c	33	8.910.0	BF173847	BF173847	1029	BF173847	BF173847
c	34	8.99.6	BF137533	BF137533	828	BF137533	BF137533
c	35	8.99.5	BF137533	BF137533	145	BF137533	BF137533
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c	37	8.99.5	BF137533	BF137533	1059	BF137533	BF137533
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c	142	8.99.3	BF137533	BF137533	1059	BF137533	BF137

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REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 304)	
AUTHORS	Ottenthaler, B., Obermaier, B., Newes, H.W., Gassnerhuber, J. and Wiemann, S.	
TITLE	EST (Ottenthaler, et al.)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Ottenthaler B	
FEATURES	MIPS Am Klopferspitz, 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No 51 sequence available. This clone (DKFZP586J0421) is available at the RZPD in Berlin-Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.	
BASE COUNT	Location/Qualifiers 1..304 /organism="Homo sapiens" /db_xref="taxon:9006" /clone="DKFZP586J0421" /clone_lib="586 (synonym: hutel)" /tissue_type="uterus" /dev_stage="adult" /lab_host="DH10B" /note="vector: pSPORT1; Site_1: NotI; site_2: Sall/MLuI" source 1..304 a 68 c 80 g 70 t	
ORIGIN		
RESULT	3	
LOCUS	BF102859	851 bp mRNA
DEFINITION	6016468271 NIH_MGC_60	EST 19-OCT-2000 mRNA sequence.
ACCESSION	BF102859	
VERSION	BF102859.1	GI:10885385
KEYWORDS		EST.
SOURCE	human	
ORGANISM	Human	
	Eukaryota	
	Metazoa	
	Chordata	
	Craniata	
	Vertebrata	
	Euteleostomi	

## Best Available Copy

ACCESSION	mRNA sequence.	LOCUS	BF021679	523 bp	mRNA	EST	29-DEC-2000
VERSION	BF031624	DEFINITION	uy5050.y1	NC_1CGAP_Lu30	Mus musculus	cDNA clone	IMAGE:3663009 5'
KEYWORDS	EST.	similar to TR_Q9OY71 Q9OY71 FALLOEIN.					
SOURCE	human.	ACCESSION	BF021679				
ORGANISM	Homo sapiens	VERSION	BF021679.1				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo	KEYWORDS	EST.				
AUTHORS	NIH-MGC	ORGANISM	Mus musculus				
TITLE	http://mgc.nci.nih.gov/	COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
JOURNAL	Unpublished (1999)	REFERENCE	1 (bases 1 to 523)				
COMMENT	Contact: Robert Strausberg, Ph.D.	AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.			
	Email: cgraphs-r@mail.nih.gov	TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).				
		JOURNAL	Tumor Gene Index				
		COMMENT	Unpublished (1997)				
			Contact: Robert Strausberg, Ph.D.				
			Email: cgraphs-r@mail.nih.gov				
			Tissue Procurement: Gilbert Smith, Ph.D.				
			cDNA Library Preparation: Life Technologies, Inc.				
			cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)				
			DNA Sequencing by: Washington University Genome Sequencing Center				
			Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: image.llnl.gov/image/html/resources.shtml				
FEATURES	Location/Qualifiers	FEATURES	MG:1423777				
	1. <i>organism</i> ="Homo sapiens"	source	Seq primer: -40RP from Gibco				
	/db_xref="taxon:9606"		High quality sequence stop: 452.				
	/clone="IMAGE:3827760"		Location/Qualifiers				
	/clone_lib="NIH_MGC_58"		1. .523				
			/organism="Mus musculus"				
			/strain="CZECH II"				
			/db_xref="taxon:10090"				
			/clone="IMAGE:3663009"				
			/clone_lib="NCI_GAP_Lu30"				
			/tissue_type="tumor, metastatic to mammary"				
			/lab_host="DH10B"				
			/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; site_2: SalI; transgenic model: WNT1; expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"				
BASE COUNT		BASE COUNT	143 a	116 c	139 g	125 t	
ORIGIN		ORIGIN					
Query Match	78 88;	Query Match	76 28;	Query Match	274 2;	Query Match	523;
Best Local Similarity	99.3%	Best Local Similarity	85.2%	Best Local Similarity	85.2%	Best Local Similarity	85.2%
Matches	285;	Matches	306;	Matches	53;	Matches	0;
Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	74	Qy	1	Qy	60	Qy	180
Db	1	Db	164	Db	223	Db	343
Qy	134	Qy	61	Qy	120	Qy	240
Db	61	Db	224	Db	283	Db	404
Qy	194	Qy	121	Qy	181	Qy	301
Db	121	Db	284	Db	344	Db	464
Qy	254	Qy	121	Qy	181	Qy	301
Db	181	Db	284	Db	344	Db	464
Qy	314	Qy	121	Qy	181	Qy	301
Db	241	Db	284	Db	344	Db	464
RESULT	5	RESULT	5	RESULT	5	RESULT	5
BF021679		BF021679		BF021679		BF021679	

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RESULT	6	LOCUS	BG69411	556 bp mRNA	EST	17-APR-2001
DEFINITION		DEFINITION	3323251 MARC 1PIG Sus scrofa cDNA 5'	mRNA sequence.		
ACCESSION	BG69411	VERIFICATION	GI:13659390			
KEYWORDS	EST.					
SOURCE	P19.					
ORGANISM	Sus scrofa					
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suis; Suidae; Sus.	7	RESULT			
AUTHORS	1 (bases 1 to 556)	LOCUS	BF151355	564 bp mRNA	EST	29-DEC-2000
VERSION	Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.	DEFINITION	BF151355	similar to TR-Q9QY71 Q9QY71 FALLOTEIN.	EST clone	IMAGE:3669119 5'
KEYWORDS	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine	ACCESSION	BF151355	;	mRNA sequence.	
SOURCE	Unpublished (2000)	KEYWORDS	BF151355.1	EST.		
ORGANISM	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine	SOURCE	house mouse.	house mouse.		
REFERENCE	Upublished (2000)	ORGANISM	Mus musculus			
AUTHORS	Smith, T.P.L., Casas, E., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.	DEFINITION	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.			
TITLE	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine	REFERENCE	1 (bases 1 to 564)			
JOURNAL	Unpublished (2000)	AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
COMMENT	Contact: Smith TPL	TITLE	National Cancer Institute, Cancer Genome Anatomy project (CGAP), Tumor Gene Index			
JOURNAL	USDA, ARS, US Meat Animal Research Center	JOURNAL	Unpublished (1997)			
COMMENT	PO Box 166, Clay Center, NE 68933-0166, USA	COMMENT	Contact: Robert Straussberg, Ph.D.			
TELEPHONE	402 762 4366	COMMENT	Email: cgaps@mail.nih.gov			
FAX	402 762 4390	COMMENT	Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys			
EMAIL	smith@email.marc.usda.gov	COMMENT	CDNA Library Preparation: Life Technologies, Inc.			
Single pass sequencing. Bases called and alt_trimmed with phred	Single pass sequencing. Bases called and alt_trimmed with phred	COMMENT	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (L1L1L1)			
0.98094 e. Vector identified by cross_match with the -minscore 18	0.98094 e. Vector identified by cross_match with the -minscore 18	COMMENT	DNA Sequencing by: Washington University Genome Sequencing Center			
and -minmatch 12 options.	and -minmatch 12 options.	COMMENT	Clone distribution by: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/L1L1L1 at: image.lnl.gov/image/html/resources.shtml			
PCR PRIMERS	FORWARD: AGGAAACAGCTTGTGACCAT BACKWARD: GTTTTCCOAGTCACGACGACG	FEATURES	MGI:14298887			
PCR PRIMERS	Plate: 98	source	Seq Primer: -40R from Gibco			
PCR PRIMERS	row: P column: 8	source	High quality sequence stop: 436.			
PCR PRIMERS	Seq primer: ATTAGCTGACCTATAG.	source	Location/Qualifiers			
PCR PRIMERS	Location/Qualifiers	1. .556	1. .564			
PCR PRIMERS	1. .556	source	/organism="Mus musculus"			
PCR PRIMERS	/organism="Sus scrofa"	source	/strain="C57/B6"			
PCR PRIMERS	/db_xref="taxon:9823"	source	/db_xref="taxon:10090"			
PCR PRIMERS	/clone_lib="MARC 1PIG"	source	/clone="IMAGE:3669119"			
PCR PRIMERS	/tissue_type="pooled"	source	/clone_lib="NCI-CGAP_Mam5"			
PCR PRIMERS	/lab_host="DH10B"	source	/tissue_type="tumor, gross tissue"			
PCR PRIMERS	/note="Vector: PCMV SP076; Site_1: xbaI; Site_2: XbaI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."	source	/dev_stage="7 months"			
PCR PRIMERS	139 a 153 c 141 g 123 t	source	/lab_host="DH10B"			
PCR PRIMERS	FEATURES	source	/note="Organ: mammary; Vector: PCMV-SP076; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"			
PCR PRIMERS	source	source	BASE COUNT	157 a	130 c	140 g
PCR PRIMERS	source	source	ORIGIN	137 t		
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
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PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
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PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
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PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
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PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
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PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
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PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
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PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
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PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
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PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
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PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
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PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
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PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
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PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
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PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
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PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels 0; Gaps 0
PCR PRIMERS	source	source	Query Match	72.7%	Score 261.8;	DB 145; Length 564;
PCR PRIMERS	source	source	Best Local Similarity	83.9%	Pred. No. 3.9e-7;	
PCR PRIMERS	source	source	Matches 296;	Conservative 0;	Mismatches 57;	Indels

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Qy	121	acggatccattttttggccaaatgggttccatggtaacgtgt	165
Db	280	ACAGATACCATATCTGGCCAGGTGTCCTCTGGTAAAGGCCTT	324

Search completed: July 18, 2001, 03:49:55  
Job time: 13553 sec